1

SEQUENCE LISTING

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<130> UF-371XC1 PCT

<150> US 60/496,188

<151> 2003-08-18

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Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys 50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp 65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val 85 90 95

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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

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Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val 145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr 165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met 195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys 210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu 225 230 235 240

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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe 260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser 275 280 285

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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys 305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr 325 330 . 335

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Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile 355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile 370 375 380

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Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly 405 410 415

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WO 2005/019425

6

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Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile 65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr 85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu 115 120 125

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Gly	, PAS	Asr	Ser 420	_	: Ile	Arg	Arg	Ala 425		e Ile	Asp	Lys	430		Arg
Ile	e Gly	435		val	. Lys	: Ile	Leu 440		Ala	a Asp	Asn	Val 445		a Glu	Ala
Ala	Met		ı Thr	. Asp	Gly	r Tyr 455		: Ile	ь Гув	s Gly	Gly 460		val	l Thr	Val

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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr 180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu 195 200 205

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WO 2005/019425

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11

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cagccaattc caaagcgtga caaagccgct gcaaatgatt caagarcatg yctcaatcct 120
caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac 180
cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt 240
gatattcctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa 300
tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg 360
tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac 420

tggtttcagg	gtactgcaga	tgctgtaagg	cagtacttgt	ggttgtttga	ggagcataat	480
gtgatggaat	ttctaattct	tgctggcgat	cacctgtacc	ggatggacta	tgaaaagttc	540
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gctgagaaac	cgaaaggaga	gcagttgaaa	gcaatgatgg	ttgacaccac	catacttggc	720
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Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly 35 40 45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys 50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile 65 70 75 80

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<211> 476

<212> PRT

<213> Mutant Bt2 protein

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Val	Leu 130	Ala	Ala	Gln	Gln	Ser 135	Pro	Asp	Asn	Pro	Asn 140	Trp	Phe	Gln	Gly
Thr 145	Ala	Asp	Ala	Val	Arg 150	Gln	Tyr	Leu	Trp	Leu 155	Phe	Glu	Glu	His	Asn 160
Val	Met	Glu	Phe	Leu 165	Ile	Leu	Ala	Gly	Asp 170	His	Leu	Tyr	Arg	Met 175	Asp
Tyr	Glu	ГÀз	Phe 180	Ile	Gln	Ala	His	Arg 185	Glu	Thr	Asn	Ala	Asp 190	Ile	Thr
Val	Ala	Ala 195	Leu	Pro	Met	Asp	Glu 200	ГХв	Arg	Ala	Thr	Ala 205	Phe	Gly	Leu
Met	Lys 210	Ile	Asp	Glu	Glu	Gly 215	Arg	Ile	Ile	Glu	Phe 220	Ala	Glu	Lys	Pro
Lys 225	Gly	Glu	Gln	Leu	Lys 230	Ala	Met	Met	Val	Asp 235	Thr	Thr	Ile	Leu	Gly 240
Leu	Asp	Asp	Val	Arg 245	Ala	Lys	Glu	Met	Pro 250	Tyr	Ile	Ala	Ser	Met 255	Gly
Ile	Tyr	Val	Phe 260	Ser	Lys	Asp	Val	Met 265	Leu	Gln	Leu	Leu	Arg 270	Glu	Gln
Phe	Pro	Glu 275	Ala	Asn	qaA	Phe	Gly 280	Ser	Glu	Val	Ile	Pro 285	Gly	Ala	Thr
Ser	Ile 290	Gly	Lys	Arg	Val	Gln 295	Ala	Tyr	Leu	Tyr	Asp 300	Gly	Tyr	Trp	Glu
Asp 305	Ile	Gly	Thr	Ile	Ala 310	Ala	Phe	Tyr	Asn	Ala 315		Leu	Gly	Ile	Thr 320
Lys	Lys	Pro	Ile	Pro 325	Asp	Phe	Ser	Phe	Туr 330	Asp	Arg	Phe	Ala	Pro 335	Ile
Tyr	Thr	Gln	Pro 340	Arg	His	Leu	Pro	Pro 345	Ser	Lys	Val	Leu	Asp 350	Ala	Asp
Val	Thr	Asp 355		Val	Ile	Gly	Glu 360	Gly	Cys	Val	Ile	ьуs 365		СЛа	Lys
Ile	Asn 370		Ser	Val	Val	Gly 375		Arg	Ser	Сув	Ile 380		Glu	Gly	Ala
Ile 385		Glu	Asp	Ser	Leu 390		Met	Gly	Ala	Asp 395		Tyr	Glu	Thr	Glu 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile 410 405 Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg 425 Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala 440 Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val 460 455 Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile 470 <210> 11 <211> 1582 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (1368) <223> r = a or g; amino acid 453 = Pro. <221> variation <222> (1578) <223> k = g or t.<400> 11 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat

243

WO 2005/019425

Сув	Pro	Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	
				cgt Arg								Gly				291
				cct Pro												339
				tac Tyr 115												387
				aat Asn												435
				cat His												483
ttt Phe	gct Ala 160	gat Asp	gga Gly	tct Ser	gta Val	cag Gln 165	gta Val	tta Leu	gcg Ala	gct Ala	aca Thr 170	caa Gln	atg Met	cct Pro	gaa Glu	531
				tgg Trp												579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
				Gly												6,75
gtg Val	cag Gln	aaa Lys 225	His	gtc Val	Glu	Asp	Asp	gct Ala	Asp	Ile	act Thr	ata Ile 235	Ser	tgt Cys	gct Ala	723
cct Pro	gtt Val 240	Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	ggg Gly	cta Leu 250	Val	aag Lys	att Ile	gat Asp	771
cat His 255	Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	Gln	tto Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	Val	gag	acc Thr	aac Asn	ttc Phe 280	: Lev	g ago L Ser	tat Tyr	gct Ala	ata Ile 285	gat Asp	867
gat Asp	gca Ala	. cag . Gln	aaa Lys 290	Туг	cca Pro	tac Tyr	ctt Lev	gca Ala 295	Ser	atg Met	: Gl ^y	att Ile	tate Tyr	. Val	ttc Phe	915

16

aag Lys	aaa Lys	gat Asp 305	gca Ala	ctt Leu	tta Leu	gac Asp	ctt Leu 310	ctc Leu	aag Lys	tca Ser	aaa Lys	tat Tyr 315	act Thr	caa Gln	tta Leu	963
cat His	gac Asp 320	ttt Phe	gga Gly	tct Ser	gaa Glu	atc Ile 325	ctc Leu	cca Pro	aga Arg	gct Ala	gta Val 330	cta Leu	gat Asp	cat His	agt Seŕ	1011
gtg Val 335	cag Gln	gca Ala	tgc Cys	att Ile	ttt Phe 340	acg Thr	gly	tat Tyr	tgg Trp	gag Glu 345	gat Asp	gtt Val	gga Gly	aca Thr	atc Ile 350	1059
aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
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tca Ser	gat Asp 400	ggt Gly	tgc Cys	tta Leu	ctg Leu	aga Arg 405	gaa Glu	tgc Cys	aac Asn	atc Ile	gag Glu 410	cat His	tct Ser	gtg Val	att Ile	1251
gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
atg Met	atg Met	gga Gly	gcg Ala	gac Asp 435	Ile	tat Tyr	gaa Glu	act Thr	gaa Glu 440	Glu	gaa Glu	gct Ala	tca Ser	aag Lys 445	cta Leu	1347
ctg Leu	tta Leu	gct Ala	999 Gly 450	Lys	gtc Val	ccr Pro	gtt Val	gga Gly 455	Ile	gga Gly	agg Arg	aac Asn	aca Thr 460	Lys	ata Ile	1395
agg Arg	aac Asn	tgt Cys 465	Ile	att Ile	gac Asp	atg Met	aat Asn 470	Ala	agg Arg	att Ile	. Gly	aag Lys 475	Asn	gtg Val	gtg Val	1443
ato Ile	aca Thr 480	Asr	agt Ser	aag Lys	gly ggc	ato Ile 485	Glr	gag Glu	gct Ala	gat Asp	Cac His 490	Pro	gaa Glu	gaa Glu	gly aga	1491
tac Tyr 495	Ser	tac Tyr	tac Tyr	ata Ile	agg Arg 500	g Ser	: gga	ato Ile	gto Val	gtg Val 505	. Ile	c ctg E Lev	, aag Lys	aat Asr	gca Ala 510	1539
					/ Sei	gto Val			gatog	gct	gcgt	ktgo	g			1582

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<212> PRT

<213> Zea mays

<400> 12

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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

18

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
500 505 510

Asn Asp Gly Ser Val Ile 515

<210> 13

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

<221> variation

<222> (267) <223> k = g or t; amino acid 86 = Ala. <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1368) $\langle 223 \rangle$ r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.<400> 13 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu 20 15 agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe 35 40 ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala 50 55 tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 70 291 get gat gea aac egt gta tet gek ate att ttg gge gga gge aet gga Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 105 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 120 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 135 tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn 150

					gta Val											531
gag Glu 175	cca Pro	gct Ala	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
gta Val	atc Ile	ttg Leu	agt Ser 210	ggc	gat Asp	cag Gln	ctt Leu	tat Tyr 215	cgg Arg	atg Met	aat Asn	tac Tyr	atg Met 220	gaa Glu	ctt Leu	675
gtg Val	cag Gln	aaa Lys 225	cat His	gtc Val	gag Glu	gac Asp	gat Asp 230	gct Ala	gat Asp	atc Ile	act Thr	ata Ile 235	tca Ser	tgt Cys	gct Ala	723
					cga Arg											771
cat His 255	act Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	cca Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	gtt Val	gag Glu	acc Thr	aac Asn	ttc Phe 280	ctg Leu	agc Ser	tat Tyr	gct Ala	ata Ile 285	Asp	867
gat Asp	gca Ala	cag Gln	aaa Lys 290	Tyr	cca Pro	tac Tyr	ctt Leu	gca Ala 295	Ser	atg Met	ggc	att Ile	tat Tyr 300	gtc Val	ttc Phe	915
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cat His	gac Asp 320	Phe	gga Gly	tct Ser	gaa Glu	atc Ile 325	Leu	cca Pro	aga Arg	gct	gta Val 330	Leu	gat Asp	tay Tyr	agt Ser	1011
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tto Lev	g cct L Pro	cco Pro	g acc	g caa Glr	a ttg n Lev	gac L Asp	aaç Lys	g tgo s Cys	aaç Lys	ato Met	g aaa Lys	tat Tyr	gca Ala	ttt Phe	atc lle	1203

		385					390					395				
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gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	agc Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	ctc Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
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Tyr							gga Gly									1539
495																
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acc Thr <21 <21 <21 <40 Met	Ile 0> 1 1> 5 2> P 3> Z 0> 1 Gln	Asn 4 18 RT ea m 4	Asp ays Ala	Leu SGly	Ser	Val	Ile	Thr	Asn 10	Ser	· Gly	· Pro	His	15 Ser		1582
acc Thr <21 <21 <21 <40 Met 1	11e 0	Asn 4 18 RT ea m 4 Phe	Asp ays Ala Glu 20 Lys	Leu 5 Gly	Ala	Leu	Asp	Thr Asp 25	Asn 10 Arg	Ser	Gly Glu	Pro . Lys	His Leu 30	15 Ser		1582
acc Thr <21 <21 <21 <40 Met 1 Arg	Ile 0 > 1 1 > 5 2 > P 3 > Z 0 > 1 Gln Ser	Asn 4 18 RT ea m 4 Phe Cys Arg 35 Ala	Asp ays Ala Glu 20 Lys	Leu 5 Gly	Ala Asp	Leu Gly Lys	Asp Ile Ala 40	Thr Asp 25 Leu	Asn 10 Arg	Ser Leu Asr	Gly Glu Arg	Pro Lys Cys 45	His Leu 30	15 Ser	lle	1582
acc Thr <21 <21 <21 <40 Met 1 Arg Gly	Thr	Asn 4 18 RT ea m 4 Phe Cys Arg 35 Ala	Asp ays Ala Glu 20 Lys	Leu 5 Gly Gln	Ala Asp Glu	Leu Gly Lys Gln 55	Asp Ile Ala 40	Thr Asp 25 Leu	Asn 10 Arg	Ser Leu Asn	Gly Glu Arg Ser 60	Pro Lys Cys 45	His Leu 30 Phe	Ser Gly Cys	lle Gly	1582

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly 105 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 120 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 185 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 200 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 215 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 230 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 265 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala , 280 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 365 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val

23

405 410 415 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 470 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 505 Asn Asp Gly Ser Val Ile 515 <210> 15 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala.<220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1368) $\langle 223 \rangle$ r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.<400> 15 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His 10

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											aga Arg					147
											ctt Leu					195
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WO 2005/019425

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cat His	gac Asp 320	ttt Phe	gga Gly	tct Ser	gaa Glu	atc Ile 325	ctc Leu	cca Pro	aga Arg	gct Ala	gta Val 330	cta Leu	gat Asp	tay Tyr	agt Ser	1011
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gga Gly 415	val	tgc Cys	tca Ser	cgt Arg	gto Val 420	Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	. Leu	aag Lys	Asp Asp	tcc Ser	gtg Val 430	1299
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cto Lev	j tta i Lev	gct Ala	999 G Gly	, PA	gto Val	ccr Pro	gtt Val	gga L Gl _y 455	r Ile	. Gl?	a agg / Arg	g aac g Asr	aca Thr 460	: Гу	g ata s Ile	1395
agg Arg	g aac g Asr	tgi Cyi 46	s Ile	atte Ile	gad Bag	ato Met	g aat : Asi 470	n Ala	agg Arg	g att g Ile	e Gly	д аад 7 Буз 475	a Ası	gtg n Val	g gtg L Val	1443

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490											
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510											
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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 280 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 315 310 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp Gly Ser Val Ile

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<223> Shrunken-2 gene revertant form, modified to be
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<223> k = g \text{ or t; amino acid } 86 = Ala.
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<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.
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<222> (1008)
<223> y = c or t.
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<222> (1368)
<223> r = a \text{ or } g; \text{ amino acid } 453 = Pro.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
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Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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											cag Gln					435
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											tcc Ser					627
											aat Asn			Glu		675
								Ala			act Thr					723
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	Thr					Gln					cca Pro					819
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															tta Leu	963

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															ata Ile,	1395
								Ala					Asn		gtg Val	1443
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tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	atc Ile	Leu 505	. Lys	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
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<213> Zea mays

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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
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Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu 435 . 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

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<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

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<223> y = c or t.
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<222> (1209)
<223> y = c or t.
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\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
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<222> (1371)
<223> h = a or c or t/u.
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<223> k = g or t.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
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Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
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				gta Val												819
				aga Arg 275	Val					Leu					Asp	867
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WO 2005/019425 PCT/US2004/026965

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

WO 2005/019425

36

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37

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His 390 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 410 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 420 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu 440 Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 21 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (321) <223> n = a or g or c or t/u, unknown, or other. <220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation

WO 2005/019425

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tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 70 65

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tot cag etc ttt cet etg aca age aca acn get acg ect get gta ect 339 Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro 100

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gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627

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WO 2005/019425

40

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44

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Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510

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Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

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Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

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Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 435 440 445

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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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gta Val	atc Ile	ttg Leu	agt Ser 210	ggc	gat Asp	cag Gln	ctt Leu	tat Tyr 215	ccn Pro	atg Met	aat Asn	tac Tyr	atg Met 220	Glu	ctt Leu	675
gtg Val	cag Gln	aaa Lys 225	His	gtc Val	gag Glu	gac Asp	gat Asp 230	Ala	gat Asp	atc Ile	act Thr	ata Ile 235	Ser	tgt Cys	gct Ala	723
cct Pro	gtt Val 240	Asp	gag Glu	ago Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	Gly 333	cta Leu 250	Val	aag Lys	ı att : Ile	gat Asp	771
cat His 255	Thr	gly gga	cgt Arc	gta Val	ctt Leu 260	Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt ggt	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	ato Met	aga Arc 275	y Val	gag Glu	acc Thr	aac Asn	tto Phe 280	Let	g ago ı Ser	tat Tyr	gct Ala	ata 11e 285	gat Asp	867
gat Asp	gca Ala	caç Glr	g aaa 1 Lys 290	з Туз	cca Pro	tac Tyr	ctt Lei	gca Ala 295	. Ser	atg Met	: Gl ⁷ 3 330	att / Ile	tate Tyr	c Val	ttc Phe	915
aag Lys	aaa Lys	a gat 309	, Ala	a ctt a Lei	tta 1 Lei	a gad 1 Asp	ctt Let 310	ı Let	c aag ı Lys	g tca Sei	a aaa c Lys	a tat 31!	Th	t caa r Glr	tta Leu	963
cat His	gad 320	Phe	t gga e Gl	a tct y Sei	gaa Glu	a ato 1 Ile 325	e Le	e cca	a aga o Arg	a gci g Ala	t gta a Val 330	l Le	a gat u Asj	t tay p Tyi	y agt c Ser	1011

gtg Val 335	cag Gln	gca Ala	tgc Cys	att Ile	ttt Phe 340	acg Thr	ggc Gly	tat Tyr	tgg Trp	gag Glu 345	gat Asp	gtt Val	gga Gly	aca Thr	atc Ile 350	1059
aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
ttt Phe	gat Asp	ttt Phe	tac Tyr 370	gat Asp	cca Pro	aaa Lys	aca Thr	cct Pro 375	ttc Phe	ttc Phe	act Thr	gca Ala	ccc Pro 380	cga Arg	tgc Cys	1155
ttg Leu	cct Pro	ccg Pro 385	acg Thr	caa Gln	ttg Leu	gac Asp	aag Lys 390	tgc Cys	aag Lys	atg Met	aaa Lys	tat Tyr 395	gca Ala	ttt Phe	atc Ile	1203
tca Ser	gat Asp 400	ggt Gly	tgc Cys	tta Leu	ctg Leu	aga Arg 405	gaa Glu	tgc Cys	aac Asn	atc Ile	gag Glu 410	cat His	tct Ser	gtg Val	att Ile	1251
gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	agc Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	ctc Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
atg Met	atg Met	gga Gly	gcg Ala	gac Asp 435	atc Ile	tat Tyr	gaa Glu	act Thr	gaa Glu 440	Glu	gaa Glu	gct Ala	tca Ser	aag Lys 445	cta Leu	1347
ctg Leu	tta Leu	gct Ala	999 Gly 450	aag Lys	gtc Val	ccr Pro	gtt Val	gga Gly 455	ata Ile	gga Gly	agg Arg	aac Asn	aca Thr 460	Lys	ata Ile	1395
agg Arg	aac Asn	tgt Cys 465	Ile	att Ile	gac Asp	atg Met	aat Asn 470	Ala	agg Arg	att Ile	gly	aag Lys 475	Asn	gtg Val	gtg Val	1443
atc Ile	aca Thr 480	Asn	agt Ser	aag Lys	ggc	atc Ile 485	Gln	gag Glu	gct Ala	gat Asp	cac His	Pro	gaa Glu	gaa Gl'u	Gly 999	1491
tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	ato Ile	ctg Lev 505	Lys	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
					ata Ile		atcg	ıgct	gcgt	ktgc:	g ,					1576

<210> 26

<211> 516

<212> PRT

<213> Zea mays

<400> 26

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1 5 10 15

Arg	Ser	Сув	Glu 20	Gly	Asp	Gly	Ile	Asp 25	Arg	Leu	Glu	Lys	Leu 30	Ser	Ile
Gly	Gly	Arg 35	Lys	Gln	Glu	ГÀа	Ala 40	Leu	Arg	Asn	Arg	Cys 45	Phe	Gly	Gly
Arg	Val 50	Ala	Ala	Thr	Thr	Gln 55	Сув	Ile	Leu	Thr	Ser 60	Asp	Ala	СЛв	Pro
Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	Ala	Asp 80
Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	Ser 95	Gln
Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg	Ala 105	Thr	Pro	Ala	Val	Pro 110	Val	Gly
Gly	Сув	Tyr 115	Arg	Leu	Ile	Asp	Ile 120	Pro	Met	Ser	Asn	Cys 125	Phe	Asn	Ser
Gly	Ile 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	Gln	Phe	Asn 140	Ser	Thr	Ser	Leu
Asn 145	Arg	His	Ile	His	Arg 150	Thr	Tyr	Leu	Glu	Gly 155	Gly	Ile	Asn	Phe	Ala 160
Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
Ala	Gly	Trp	Phe 180	Gln	Gly	Thr	Ala	Asp 185	Ser	,Ile	Arg	Lys	Phe 190	Ile	Trp
Val	Leu	Glu 195		Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205		Val	Ile
Leu	Ser 210		Asp	Gln	Leu	Tyr 215		Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225		Val	. Glu	Asp	Asp 230		Asp	Ile	Thr	1le 235		Cys	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245		Lys	Asn	Gly	Leu 250		Lys	Ile	Asp	His 255	Thr
Gly	Arg	Val	Leu 260		Phe	Phe	Glu	Lys 265		Lys	Gly	Ala	Asp 270		Asn
Ser	. Met	275		. Glu	Thr	Asn	Phe 280		Ser	Tyr	Ala	. Ile 285		Asp	Ala
Glr	Lys 290		r Pro	туг	Leu	Ala 295		Met	: Gly	7 Ile	300		. Phe	: Lys	Lys
Asp 305		Let	ı Lev	ı Asp	310		. Lys	Ser	. PAS	315		Glr	Lev	. His	320
			- 01.	1-		. n	7~~	. א ז -	TC-17	T.O.) Acr	Tree	- 601	- 17a1	Gln

335 325 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp . 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu 440 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 470 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 485 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 500 Gly Ser Val Ile 515

<210> 27

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS ·

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1287) <223> y = c or t.<220> <221> variation <222> (1368) $\langle 223 \rangle$ r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His 99 cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe 195 ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly 80 85 tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 95 100 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 115 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 130

WO 2005/019425

tcg Ser	ctt Leu	aac Asn 145	cgc Arg	cat His	att Ile	cat His	cgt Arg 150	aca Thr	tac Tyr	ctt Leu	gaa Glu	ggc Gly 155	gjå aaa	atc Ile	aac Asn	483
ttt Phe	gct Ala 160	gat Asp	gga Gly	tct Ser	gta Val	cag Gln 165	gta Val	tta Leu	gcg Ala	gct Ala	aca Thr 170	caa Gln	atg Met	cct Pro	gaa Glu	531
gag Glu 175	cca Pro	gtn Val	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	ааа Lув	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
gta Val	atc Ile	ttg Leu	agt Ser 210	ggc Gly	gat Asp	cag Gln	ctt Leu	tat Tyr 215	cgg Arg	atg Met	aat Asn	tac Tyr	atg Met 220	gaa Glu	ctt Leu	675
gtg Val	cag Gln	aaa Lys 225	cat His	gtc Val	gag Glu	gac Asp	gat Asp 230	gct Ala	gat Asp	atc Ile	act Thr	ata Ile 235	tca Ser	tgt Cys	gct Ala	723
cct Pro	gtt Val 240	gat Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	tct Ser	aaa Lys	aat Asn	GJ A GGG	cta Leu 250	gtg Val	aag Lys	att Ile	gat Asp	771
cat His 255	Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
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gat Asp	gca Ala	cag Gln	aaa Lys 290	Tyr	cca Pro	tac Tyr	ctt Leu	gca Ala 295	Ser	atg Met	ggc Gly	att Ile	tat Tyr 300	Val	ttc Phe	915
aag Lys	aaa Lys	gat Asp 305	Ala	ctt Leu	tta Leu	gac Asp	ctt Leu 310	Leu	aag Lys	tca Ser	aaa Lys	tat Tyr 315	Thr	caa Gln	tta Leu	963
cat His	gac Asp 320	Phe	: Gly	tct Ser	gaa Glu	ato Ile 325	e Lev	cca Pro	aga Arg	gct Ala	gta Val 330	. Lev	gat Asp	cay His	agt Ser	1011
gtg Val 335	. Glr	gca Ala	tgo Cys	att Ile	ttt Phe 340	Thi	Gly Ggg	tat Tyr	tgg Tr	gag Glu 345	ı Ası	gtt Val	gga . Gly	aca Thr	atc : Ile 350	1059
ааа ҍуя	tca Sei	tto Phe	ttt Phe	gat Asp 355	Ala	ı aad Ası	ttg Lei	g gcc ı Ala	cto Leu 360	ı Thi	gag Glu	g cag ı Glr	g cct n Pro	tco Ser 365	aag Lys	1107
ttt Phe	gat Asp	ttt Phe	tac Ty:	c Asp	cca Pro	a aaa b Lys	a aca 3 Thi	e cct Pro 375	Phe	tto Phe	c act	gca Ala	a ccc a Pro 380) Arg	a tgc J Cys	1155

ttg Leu	cct Pro	ccg Pro 385	acg Thr	caa Gln	ttg Leu	gac Asp	aag Lys 390	tgc Cys	aag Lys	atg Met	aaa Lys	tat Tyr 395	gca Ala	ttt Phe	atc Ile	1203
tca Ser	gat Asp 400	ggt Gly	tgc Cys	tta Leu	ctg Leu	aga Arg 405	gaa Glu	tgc Cys	aac Asn	atc Ile	gag Glu 410	cat His	tct Ser	gtg Val	att Ile	1251
gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	agc Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	tty Phe	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
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ctg Leu	tta Leu	gct Ala	999 Gly 450	aag Lys	gtc Val	ccr Pro	gtt Val	gga Gly 455	ata Ile	gga Gly	agg Arg	aac Asn	aca Thr 460	aag Lys	ata Ile	1395
agg Arg	aac Asn	tgt Cys 465	atc Ile	att Ile	gac Asp	atg Met	aat Asn 470	gct Ala	agg Arg	att Ile	gl ^à aaa	aag Lys 475	aac Asn	gtg Val	gtg Val	1443
atc Ile	aca Thr 480	aac Asn	agt Ser	aag Lys	ggc	atc Ile 485	caa Gln	gag Glu	gct Ala	gat Asp	cac His 490	ccg Pro	gaa Glu	gaa Glu	Gly 999	1491
tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	atc Ile	ctg Leu 505	Lys	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
				gtc Val 515	Ile		atcg	gct	gcgt	ktgc	g					1576

<210> 28

<211> 516

<212> PRT

<213> Zea mays

<400> 28

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80

WO 2005/019425

- Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 · 95
- Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
- Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125
- Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140
- Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160
- Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175
- Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190
- Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205
- Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 220
- Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240
- Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255
- Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270
- Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285
- Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300
- Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320
- Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335
- Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350
- Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365
- Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380
- Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp

56

400 390 395 385 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met 420 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 440 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 470 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 29 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) $\langle 223 \rangle$ k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (981) <223> r = g or a.<220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1086) <223> n = a or g or c or t/u, unknown, or other. <220>

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<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.
<220>
<221> variation
<222> (1368)
<223> r = a \text{ or } g; \text{ amino acid } 453 = Pro.
<220>
<221> variation
<222> (1578)
<223> k = g or t.
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          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
                                                                    99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct
                                                                     339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                                  135
 tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
 ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
                                              170
                          165
     160
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gag Glu 175	cca Pro	gct Ala	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
gta Val	atc Ile	ttg Leu	agt Ser 210	ggc	gat Asp	cag Gln	ctt Leu	tat Tyr 215	cgg Arg	atg Met	aat Asn	tac Tyr	atg Met 220	gaa Glu	ctt Leu	675
gtg Val	cag Gln	aaa Lys 225	cat His	gtc Val	gag Glu	gac Asp	gat Asp 230	gct Ala	gat Asp	atc Ile	act Thr	ata Ile 235	tca Ser	tgt Cys	gct Ala	723
cct Pro	gtt Val 240	gat Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	tct Ser	aaa Lys	aat Asn	eja aaa	cta Leu 250	gtg Val	aag Lys	att Ile	gat Asp	771
cat His 255	act Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	cca Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
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gat Asp	gca Ala	cag Glr	aaa Lys 290	Tyr	cca Pro	tac Tyr	ctt Leu	gca Ala 295	Ser	atg Met	. Gly	att Ile	tat Tyr 300	vaı	ttc Phe	915
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cat His	gac Asp 320	Phe	gga Gly	a tct / Ser	aar Lys	ato Ile 325	Lev	cca Pro	aga Arg	gct JAla	gta Val	l Leu	gat Asp	cay His	agt Ser	1011
gto Val	. Glr	g gca n Ala	a tgo a Cy:	c att	ttt Phe	Thr	. Gl ⁷	taty Tyr	tgg Tr	g gag o Gli 34!	ı Ası	gtt Val	gga Gly	aca Thi	atc Ile 350	1059
aaa Lys	a tca 3 Sei	a tto	e tti	t gai e Ası 35!	o Ala	a aac a Ası	ttq Lei	g gti 1 Val	n cto L Len 360	1 Th	t gag r Gli	g cag u Glr	g cct n Pro	tco Ser 36!	aag Lys	1107
tt: Ph	gat Asj	t tt p Ph	t ta e Ty 37	r As	t cca p Pro	a aaa o Ly:	a aca	a cci r Pro 37	o Ph	c tto e Pho	c ac e Th	t gca r Ala	a cce a Pre 38	o Arg	a tgc g Cys	1155
tt: Le:	g cc	t cc o Pr 38	o Th	g ca r Gl:	a ttg n Lei	g ga u As	c aag p Lys 39	в Су	c aa s Ly	g at s Me	g aa t Ly	a tai s Ty: 39:	r va	n tt l Ph	t atc e Ile	1203
tc: Se:	a ga r As	t gg p Gl	t tg y Cy	c tt s Le	a ct u Le	g ag u Ar	a ga g Gl	a tg u Cy	c aa s As	c at n Il	c ga e Gl	g ca u Hi	t tc s Se	t gt r Va	g att l Ile	1251

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Cys	s Sei	c Arg	y Va]		Ser	Gly	/ Сув	Glu 425		ı Lys	as Asp	Ser	val 430	Met	Met

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25

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Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

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Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val

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. 65

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WO 2005/019425 PCT/US20

69

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PCT/US2004/026965 WO 2005/019425

78

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<223> k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.
<220>
<221> variation
<222> (1368)
<223> r = a \text{ or } g; \text{ amino acid } 453 = Pro.
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<221> variation
<222> (1578)
<223> k = g \text{ or t.}
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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                     147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                     195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
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Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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                          85
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct
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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95
                     100
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aac Asn	agt Ser	ggt Gly	ata Ile 130	aat Asn	r Pàs	ata Ile	ttt Phe	gtg Val 135	atg Met	agt Ser	cag Gln	ttc Phe	aat Asn 140	tct Ser	act Thr	435
tcg Ser	ctt Leu	aac Asn 145	cgc Arg	cat His	att Ile	cat His	cgt Arg 150	aca Thr	tac Tyr	ctt Leu	gaa Glu	ggc Gly 155	eja aaa	atc Ile	aac Asn	483
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gag Glu 175	cca Pro	gtn Val	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
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cct Pro	gtt Val 240	Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	gjå aaa	cta Leu 250	Val	aag Lys	att Ile	gat Asp	771
cat His 255	Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	Gln	tto Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt Gly	get Ala	gat Asp 270	819
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gat As <u>ı</u>	gca Ala	cag Glr	aaa 1 Lys 290	Tyr	cca Pro	tac Tyr	ctt Lev	gca Ala 295	Ser	atg Met	: Gly	att Ile	tat Tyi	· Val	ttc Phe	915
aaq Lys	g aaa s Lys	a gat 309	Ala	ı ctt ı Lei	tta Lev	gac Asp	ctt Lev 310	ı Lev	aag Lys	tca Sei	a aas C Lys	tat Tyr 315	Thi	caa Glr	tta Leu	963
ca: Hi:	t gad s Asp 320	Phe	e Gly	a tct / Sei	gaa Glu	a ato 1 Ile 325	e Let	c cca	a aga o Arg	gct g Ala	gta a Val 330	L Let	a gat 1 Asj	t tay	y agt r Ser	1011
gt: Va: 33:	1 Gl:	g gca n Ala	a tgo a Cys	c att	ttt Phe 340	e Thi	g ggo	tai Y Ty:	tgg Tr	g gag Glu 34!	ı Ası	gti Val	l Gly	a aca y Th:	a atc r Ile 350	1059

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ctg Leu	tta Leu	gct Ala	999 Gly 450	aag Lys	gtc Vaļ	ccr Pro	gtt Val	gga Gly 455	ata Ile	gga Gly	agg Arg	aac Asn	aca Thr 460	aag Lys	ata Ile	1395
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tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	atc Ile	ctg Leu 505	. Lys	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
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<212> PRT

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Gly	Ile 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	Gln	Phe	Asn 140	Ser	Thr	Ser	Leu
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Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
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Val	Leu	Glu 195	Asp	Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205	Ile	Val	Ile
Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Arg	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Сув	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245	Ser	Lys	Asn	Gly	Leu 250		Lys	Ile	Asp	His 255	Thr
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Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295		Met	Gly	Ile	Tyr 300	Val	Phe	Lys	Lys
Asp 305	Ala	Leu	Leu	ĄsĄ	Leu 310		Lys	Ser	Lys	Tyr 315		Gln	Leu	His	Asp 320
Phe	Gly	Ser	Glu	Ile 325		Pro	Arg	Ala	Val 330		Asp	Tyr	Ser	Val 335	Gln
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89

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- Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp 385 390 395 400
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- Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460
- Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480
- Asn Ser Lys Gly Ile Glu Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 485 490 495
- Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile 515